



# SEQUENCE LISTING

<110> Sundelin, Johan  
Scarborough, Robert M.

<120> Recombinant C140 Receptor, Its Agonists and Antagonists, and  
Nucleic Acids Encoding the Receptor

<130> 44481-5006-09-US

<140> US 10/643,627  
<141> 2003-08-19

<150> US 10/127,691  
<151> 2002-04-23

<150> US 08/097,938  
<151> 1993-07-26

<150> US 08/390,301  
<151> 1995-01-25

<150> US 08/474,414  
<151> 1995-06-07

<160> 64

<170> PatentIn Ver. 2.1

<210> 1  
<211> 1475  
<212> DNA  
<213> Mus musculus

<220>  
<221> CDS  
<222> (232)..(1416)  
<223> C140 receptor, genomic DNA and deduced protein  
sequences

<400> 1  
ccctgtcagt cttaagattc tagaagtcgc tgtcctatac ggaacccaaa actctcactg 60  
ttaatgaaat accattgtcg gggcgaagat gtagctcagt ggtaaaatac ttgccagcac 120  
acacaagaat tagacttcaa ccgtcaccaa ctgccctgtg taggacggtc ggtcactgaa 180  
agagaatatt gtctgcaata ctctaatac atctgtctgt gttcatctga a atg ttc 237  
Met Phe  
1  
cat tta aaa cac agc agc ctt act gtt gga cca ttt atc tca gta atg 285  
His Leu Lys His Ser Ser Leu Thr Val Gly Pro Phe Ile Ser Val Met  
5 10 15  
att ctg ctc cgc ttt ctt tgt aca gga cgc aac aac agt aaa gga aga 333  
Ile Leu Leu Arg Phe Leu Cys Thr Gly Arg Asn Asn Ser Lys Gly Arg  
20 25 30  
agt ctt att ggc aga tta gaa acc cag cct cca atc act ggg aaa ggg 381  
Ser Leu Ile Gly Arg Leu Glu Thr Gln Pro Pro Ile Thr Gly Lys Gly  
35 40 45 50  
gtt ccg gta gaa cca ggc ttt tcc atc gat gag ttc tct gcg tcc atc 429  
Val Pro Val Glu Pro Gly Phe Ser Ile Asp Glu Phe Ser Ala Ser Ile  
55 60 65  
ctc acc ggg aag ctg acc acg gtc ttt ctt ccg gtc gtc tac att att 477  
Leu Thr Gly Lys Leu Thr Thr Val Phe Leu Pro Val Val Tyr Ile Ile  
70 75 80

gtg	ttt	gtg	att	ggg	ttg	ccc	agt	aat	ggc	atg	gcc	ctc	tgg	atc	ttc	525
Val	Phe	Val	Ile	Gly	Leu	Pro	Ser	Asn	Gly	Met	Ala	Leu	Trp	Ile	Phe	
	85						90					95				
ctt	ttc	cga	acg	aag	aag	aaa	cac	ccc	gcc	gtg	att	tac	atg	gcc	aac	573
Leu	Phe	Arg	Thr	Lys	Lys	Lys	His	Pro	Ala	Val	Ile	Tyr	Met	Ala	Asn	
	100					105					110					
ctg	gcc	ttg	gcc	gac	ctc	ctc	tct	gtc	atc	tgg	ttc	ccc	ctg	aag	atc	621
Leu	Ala	Leu	Ala	Asp	Leu	Leu	Ser	Val	Ile	Trp	Phe	Pro	Leu	Lys	Ile	
	115				120					125					130	
tcc	tac	cac	cta	cat	ggc	aac	aac	tgg	gtc	tac	ggg	gag	gcc	ctg	tgc	669
Ser	Tyr	His	Leu	His	Gly	Asn	Asn	Trp	Val	Tyr	Gly	Glu	Ala	Leu	Cys	
				135					140					145		
aag	gtg	ctc	att	ggc	ttt	ttc	tat	ggg	aac	atg	tat	tgc	tcc	atc	ctc	717
Lys	Val	Leu	Ile	Gly	Phe	Phe	Tyr	Gly	Asn	Met	Tyr	Cys	Ser	Ile	Leu	
			150					155					160			
ttc	atg	acc	tgc	ctc	agc	gtg	cag	agg	tac	tgg	gtg	atc	gtg	aac	ccc	765
Phe	Met	Thr	Cys	Leu	Ser	Val	Gln	Arg	Tyr	Trp	Val	Ile	Val	Asn	Pro	
		165					170					175				
atg	gga	cac	ccc	agg	aag	aag	gca	aac	atc	gcc	gtt	ggc	gtc	tcc	ttg	813
Met	Gly	His	Pro	Arg	Lys	Lys	Ala	Asn	Ile	Ala	Val	Gly	Val	Ser	Leu	
	180					185					190					
gca	atc	tgg	ctc	ctg	att	ttt	ctg	gtc	acc	atc	cct	ttg	tat	gtc	atg	861
Ala	Ile	Trp	Leu	Leu	Ile	Phe	Leu	Val	Thr	Ile	Pro	Leu	Tyr	Val	Met	
	195				200				205					210		
aag	cag	acc	atc	tac	att	cca	gca	ttg	aac	atc	acc	acc	tgt	cac	gat	909
Lys	Gln	Thr	Ile	Tyr	Ile	Pro	Ala	Leu	Asn	Ile	Thr	Thr	Cys	His	Asp	
				215					220					225		
gtg	ctg	cct	gag	gag	gta	ttg	gtg	ggg	gac	atg	ttc	aat	tac	ttc	ctc	957
Val	Leu	Pro	Glu	Glu	Val	Leu	Val	Gly	Asp	Met	Phe	Asn	Tyr	Phe	Leu	
		230						235					240			
tca	ctg	gcc	att	gga	gtc	ttc	ctg	ttc	ccg	gcc	ctc	ctt	act	gca	tct	1005
Ser	Leu	Ala	Ile	Gly	Val	Phe	Leu	Phe	Pro	Ala	Leu	Leu	Thr	Ala	Ser	
		245					250					255				
gcc	tac	gtg	ctc	atg	atc	aag	acg	ctc	cgc	tct	tct	gct	atg	gat	gaa	1053
Ala	Tyr	Val	Leu	Met	Ile	Lys	Thr	Leu	Arg	Ser	Ser	Ala	Met	Asp	Glu	
	260					265					270					
cac	tca	gag	aac	aaa	agg	cag	agg	gct	atc	cga	ctc	atc	atc	acc	gtg	1101
His	Ser	Glu	Lys	Lys	Arg	Gln	Arg	Ala	Ile	Arg	Leu	Ile	Ile	Thr	Val	
					280					285					290	
ctg	gcc	atg	tac	ttc	atc	tgc	ttt	gct	cct	agc	aac	ctt	ctg	ctc	gta	1149
Leu	Ala	Met	Tyr	Phe	Ile	Cys	Phe	Ala	Pro	Ser	Asn	Leu	Leu	Leu	Val	
				295					300					305		
gtg	cat	tat	ttc	cta	atc	aaa	acc	cag	agg	cag	agc	cac	gtc	tac	gcc	1197
Val	His	Tyr	Phe	Leu	Ile	Lys	Thr	Gln	Arg	Gln	Ser	His	Val	Tyr	Ala	
			310					315					320			
ctc	tac	ctt	gtc	gcc	ctc	tgc	ctg	tcg	acc	ctc	aac	agc	tgc	ata	gac	1245
Leu	Tyr	Leu	Val	Ala	Leu	Cys	Leu	Ser	Thr	Leu	Asn	Ser	Cys	Ile	Asp	
		325					330					335				
ccc	ttt	gtc	tat	tac	ttt	gtc	tca	aaa	gat	ttc	agg	gat	cac	gcc	aga	1293
Pro	Phe	Val	Tyr	Tyr	Phe	Val	Ser	Lys	Asp	Phe	Arg	Asp	His	Ala	Arg	
	340					345					350					
aac	gcg	ctc	ctc	tgc	cga	agt	gtc	cgc	act	gtg	aat	cgc	atg	caa	atc	1341

Asn Ala Leu Leu Cys Arg Ser Val Arg Thr Val Asn Arg Met Gln Ile  
 355 360 365 370  
 tcg ctc agc tcc aac aag ttc tcc agg aag tcc ggc tcc tac tct tca 1389  
 Ser Leu Ser Ser Asn Lys Phe Ser Arg Lys Ser Gly Ser Tyr Ser Ser  
 375 380 385  
 agc tca acc agt gtt aaa acc tcc tac tgagctgtac ctgaggatgt 1436  
 Ser Ser Thr Ser Val Lys Thr Ser Tyr  
 390 395  
 caagcctgct tgatgatgat gatgatgatg gtgtgtgtg 1475

<210> 2  
 <211> 395  
 <212> PRT  
 <213> Mus musculus

<400> 2  
 Met Phe His Leu Lys His Ser Ser Leu Thr Val Gly Pro Phe Ile Ser  
 1 5 10 15  
 Val Met Ile Leu Leu Arg Phe Leu Cys Thr Gly Arg Asn Asn Ser Lys  
 20 25 30  
 Gly Arg Ser Leu Ile Gly Arg Leu Glu Thr Gln Pro Pro Ile Thr Gly  
 35 40 45  
 Lys Gly Val Pro Val Glu Pro Gly Phe Ser Ile Asp Glu Phe Ser Ala  
 50 55 60  
 Ser Ile Leu Thr Gly Lys Leu Thr Thr Val Phe Leu Pro Val Val Tyr  
 65 70 75 80  
 Ile Ile Val Phe Val Ile Gly Leu Pro Ser Asn Gly Met Ala Leu Trp  
 85 90 95  
 Ile Phe Leu Phe Arg Thr Lys Lys Lys His Pro Ala Val Ile Tyr Met  
 100 105 110  
 Ala Asn Leu Ala Leu Ala Asp Leu Leu Ser Val Ile Trp Phe Pro Leu  
 115 120 125  
 Lys Ile Ser Tyr His Leu His Gly Asn Asn Trp Val Tyr Gly Glu Ala  
 130 135 140  
 Leu Cys Lys Val Leu Ile Gly Phe Phe Tyr Gly Asn Met Tyr Cys Ser  
 145 150 155 160  
 Ile Leu Phe Met Thr Cys Leu Ser Val Gln Arg Tyr Trp Val Ile Val  
 165 170 175  
 Asn Pro Met Gly His Pro Arg Lys Lys Ala Asn Ile Ala Val Gly Val  
 180 185 190  
 Ser Leu Ala Ile Trp Leu Leu Ile Phe Leu Val Thr Ile Pro Leu Tyr  
 195 200 205  
 Val Met Lys Gln Thr Ile Tyr Ile Pro Ala Leu Asn Ile Thr Thr Cys  
 210 215 220  
 His Asp Val Leu Pro Glu Glu Val Leu Val Gly Asp Met Phe Asn Tyr  
 225 230 235 240  
 Phe Leu Ser Leu Ala Ile Gly Val Phe Leu Phe Pro Ala Leu Leu Thr  
 245 250 255  
 Ala Ser Ala Tyr Val Leu Met Ile Lys Thr Leu Arg Ser Ser Ala Met  
 260 265 270

Asp Glu His Ser Glu Lys Lys Arg Gln Arg Ala Ile Arg Leu Ile Ile  
 275 280 285  
 Thr Val Leu Ala Met Tyr Phe Ile Cys Phe Ala Pro Ser Asn Leu Leu  
 290 295 300  
 Leu Val Val His Tyr Phe Leu Ile Lys Thr Gln Arg Gln Ser His Val  
 305 310 315 320  
 Tyr Ala Leu Tyr Leu Val Ala Leu Cys Leu Ser Thr Leu Asn Ser Cys  
 325 330 335  
 Ile Asp Pro Phe Val Tyr Tyr Phe Val Ser Lys Asp Phe Arg Asp His  
 340 345 350  
 Ala Arg Asn Ala Leu Leu Cys Arg Ser Val Arg Thr Val Asn Arg Met  
 355 360 365  
 Gln Ile Ser Leu Ser Ser Asn Lys Phe Ser Arg Lys Ser Gly Ser Tyr  
 370 375 380  
 Ser Ser Ser Ser Thr Ser Val Lys Thr Ser Tyr  
 385 390 395

<210> 3  
 <211> 1255  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (56)..(1249)  
 <223> C140 receptor, genomic DNA and deduced protein  
 sequences

<400> 3  
 cgctccaggc ctgggtgaca gcgagaccct gtctcataaa ttaaaaaatg aataa atg 58  
 Met  
 1  
 aat gta ctt tca ttt gaa caa acc agt gtt act gct gaa aca ttt att 106  
 Asn Val Leu Ser Phe Glu Gln Thr Ser Val Thr Ala Glu Thr Phe Ile  
 5 10 15  
 tct gta atg acc ctt gtc ttc ctt tct tgt aca gga acc aat aga tcc 154  
 Ser Val Met Thr Leu Val Phe Leu Ser Cys Thr Gly Thr Asn Arg Ser  
 20 25 30  
 tct aaa gga aga agc ctt att ggt aag gtt gat ggc aca tcc cac gtc 202  
 Ser Lys Gly Arg Ser Leu Ile Gly Lys Val Asp Gly Thr Ser His Val  
 35 40 45  
 act gga aaa gga gtt aca gtt gaa aca gtc ttt tct gtg gat gag ttt 250  
 Thr Gly Lys Gly Val Thr Val Glu Thr Val Phe Ser Val Asp Glu Phe  
 50 55 60 65  
 tct gca tct gtc ctc act gga aaa ctg acc act gtc ttc ctt cca att 298  
 Ser Ala Ser Val Leu Thr Gly Lys Leu Thr Thr Val Phe Leu Pro Ile  
 70 75 80  
 gtc tac aca att gtg ttt gtg gtg ggt ttg cca agt aac ggc atg gcc 346  
 Val Tyr Thr Ile Val Phe Val Val Gly Leu Pro Ser Asn Gly Met Ala  
 85 90 95  
 ctg tgg gtc ttt ctt ttc cga act aag aag aag cac cct gct gtg att 394  
 Leu Trp Val Phe Leu Phe Arg Thr Lys Lys Lys His Pro Ala Val Ile  
 100 105 110

tac atg gcc aat ctg gcc ttg gct gac ctc ctc tct gtc atc tgg ttc	442
Tyr Met Ala Asn Leu Ala Leu Ala Asp Leu Leu Ser Val Ile Trp Phe	
115 120 125	
ccc ttg aag att gcc tat cac ata cat ggc aac aac tgg att tat ggg	490
Pro Leu Lys Ile Ala Tyr His Ile His Gly Asn Asn Trp Ile Tyr Gly	
130 135 140 145	
gaa gct ctt tgt aat gtg ctt att ggc ttt ttc tat ggc aac atg tac	538
Glu Ala Leu Cys Asn Val Leu Ile Gly Phe Phe Tyr Gly Asn Met Tyr	
150 155 160	
tgt tcc att ctc ttc atg acc tgc ctc agt gtg cag agg tat tgg gtc	586
Cys Ser Ile Leu Phe Met Thr Cys Leu Ser Val Gln Arg Tyr Trp Val	
165 170 175	
atc gtg aac ccc atg ggg cac tcc agg aag aag gca aac att gcc att	634
Ile Val Asn Pro Met Gly His Ser Arg Lys Lys Ala Asn Ile Ala Ile	
180 185 190	
ggc atc tcc ctg gca ata tgg ctg ctg att ctg ctg gtc acc atc cct	682
Gly Ile Ser Leu Ala Ile Trp Leu Leu Ile Leu Leu Val Thr Ile Pro	
195 200 205	
ttg tat gtc gtg aag cag acc atc ttc att cct gcc ctg aac atc acg	730
Leu Tyr Val Val Lys Gln Thr Ile Phe Ile Pro Ala Leu Asn Ile Thr	
210 215 220 225	
acc tgt cat gat gtt ttg cct gag cag ctc ttg gtg gga gac atg ttc	778
Thr Cys His Asp Val Leu Pro Glu Gln Leu Leu Val Gly Asp Met Phe	
230 235 240	
aat tac ttc ctc tct ctg gcc att ggg gtc ttt ctg ttc cca gcc ttc	826
Asn Tyr Phe Leu Ser Leu Ala Ile Gly Val Phe Leu Phe Pro Ala Phe	
245 250 255	
ctc aca gcc tct gcc tat gtg ctg atg atc aga atg ctg cga tct tct	874
Leu Thr Ala Ser Ala Tyr Val Leu Met Ile Arg Met Leu Arg Ser Ser	
260 265 270	
gcc atg gat gaa aac tca gag aag aaa agg aag agg gcc atc aaa ctc	922
Ala Met Asp Glu Asn Ser Glu Lys Lys Arg Lys Arg Ala Ile Lys Leu	
275 280 285	
att gtc act gtc ctg gcc atg tac ctg atc tgc ttc act cct agt aac	970
Ile Val Thr Val Leu Ala Met Tyr Leu Ile Cys Phe Thr Pro Ser Asn	
290 295 300 305	
ctt ctg ctt gtg gtg cat tat ttt ctg att aag agc cag ggc cag agc	1018
Leu Leu Leu Val Val His Tyr Phe Leu Ile Lys Ser Gln Gly Gln Ser	
310 315 320	
cat gtc tat gcc ctg tac att gta gcc ctc tgc ctc tct acc ctt aac	1066
His Val Tyr Ala Leu Tyr Ile Val Ala Leu Cys Leu Ser Thr Leu Asn	
325 330 335	
agc tgc atc gac ccc ttt gtc tat tac ttt gtt tca cat gat ttc agg	1114
Ser Cys Ile Asp Pro Phe Val Tyr Tyr Phe Val Ser His Asp Phe Arg	
340 345 350	
gat cat gca aag aac gct ctc ctt tgc cga agt gtc cgc act gta aag	1162
Asp His Ala Lys Asn Ala Leu Leu Cys Arg Ser Val Arg Thr Val Lys	
355 360 365	
cag atg caa gta tcc ctc acc tca aag aaa cac tcc agg aaa tcc agc	1210
Gln Met Gln Val Ser Leu Thr Ser Lys Lys His Ser Arg Lys Ser Ser	
370 375 380 385	
tct tac tct tca agt tca acc act gtt aag acc tcc tat tgagtt	1255

Ser Tyr Ser Ser Ser Ser Thr Thr Val Lys Thr Ser Tyr  
 390 395

<210> 4  
 <211> 398  
 <212> PRT  
 <213> Homo sapiens

<400> 4  
 Met Asn Val Leu Ser Phe Glu Gln Thr Ser Val Thr Ala Glu Thr Phe  
 1 5 10 15  
 Ile Ser Val Met Thr Leu Val Phe Leu Ser Cys Thr Gly Thr Asn Arg  
 20 25 30  
 Ser Ser Lys Gly Arg Ser Leu Ile Gly Lys Val Asp Gly Thr Ser His  
 35 40 45  
 Val Thr Gly Lys Gly Val Thr Val Glu Thr Val Phe Ser Val Asp Glu  
 50 55 60  
 Phe Ser Ala Ser Val Leu Thr Gly Lys Leu Thr Thr Val Phe Leu Pro  
 65 70 75 80  
 Ile Val Tyr Thr Ile Val Phe Val Val Gly Leu Pro Ser Asn Gly Met  
 85 90 95  
 Ala Leu Trp Val Phe Leu Phe Arg Thr Lys Lys Lys His Pro Ala Val  
 100 105 110  
 Ile Tyr Met Ala Asn Leu Ala Leu Ala Asp Leu Leu Ser Val Ile Trp  
 115 120 125  
 Phe Pro Leu Lys Ile Ala Tyr His Ile His Gly Asn Asn Trp Ile Tyr  
 130 135 140  
 Gly Glu Ala Leu Cys Asn Val Leu Ile Gly Phe Phe Tyr Gly Asn Met  
 145 150 155 160  
 Tyr Cys Ser Ile Leu Phe Met Thr Cys Leu Ser Val Gln Arg Tyr Trp  
 165 170 175  
 Val Ile Val Asn Pro Met Gly His Ser Arg Lys Lys Ala Asn Ile Ala  
 180 185 190  
 Ile Gly Ile Ser Leu Ala Ile Trp Leu Leu Ile Leu Leu Val Thr Ile  
 195 200 205  
 Pro Leu Tyr Val Val Lys Gln Thr Ile Phe Ile Pro Ala Leu Asn Ile  
 210 215 220  
 Thr Thr Cys His Asp Val Leu Pro Glu Gln Leu Leu Val Gly Asp Met  
 225 230 235 240  
 Phe Asn Tyr Phe Leu Ser Leu Ala Ile Gly Val Phe Leu Phe Pro Ala  
 245 250 255  
 Phe Leu Thr Ala Ser Ala Tyr Val Leu Met Ile Arg Met Leu Arg Ser  
 260 265 270  
 Ser Ala Met Asp Glu Asn Ser Glu Lys Lys Arg Lys Arg Ala Ile Lys  
 275 280 285  
 Leu Ile Val Thr Val Leu Ala Met Tyr Leu Ile Cys Phe Thr Pro Ser  
 290 295 300  
 Asn Leu Leu Leu Val Val His Tyr Phe Leu Ile Lys Ser Gln Gly Gln  
 305 310 315 320

Ser His Val Tyr Ala Leu Tyr Ile Val Ala Leu Cys Leu Ser Thr Leu  
325 330 335  
Asn Ser Cys Ile Asp Pro Phe Val Tyr Tyr Phe Val Ser His Asp Phe  
340 345 350  
Arg Asp His Ala Lys Asn Ala Leu Leu Cys Arg Ser Val Arg Thr Val  
355 360 365  
Lys Gln Met Gln Val Ser Leu Thr Ser Lys Lys His Ser Arg Lys Ser  
370 375 380  
Ser Ser Tyr Ser Ser Ser Ser Thr Thr Val Lys Thr Ser Tyr  
385 390 395

<210> 5  
<211> 395  
<212> PRT  
<213> Mus musculus

<220>  
<223> Protein sequence of C140 receptor

<400> 5  
Met Phe His Leu Lys His Ser Ser Leu Thr Val Gly Pro Phe Ile Ser  
1 5 10 15  
Val Met Ile Leu Leu Arg Phe Leu Cys Thr Gly Arg Asn Asn Ser Lys  
20 25 30  
Gly Arg Ser Leu Ile Gly Arg Leu Glu Thr Gln Pro Pro Ile Thr Gly  
35 40 45  
Lys Gly Val Pro Val Glu Pro Gly Phe Ser Ile Asp Glu Phe Ser Ala  
50 55 60  
Ser Ile Leu Thr Gly Lys Leu Thr Thr Val Phe Leu Pro Val Val Tyr  
65 70 75 80  
Ile Ile Val Phe Val Ile Gly Leu Pro Ser Asn Gly Met Ala Leu Trp  
85 90 95  
Ile Phe Leu Phe Arg Thr Lys Lys Lys His Pro Ala Val Ile Tyr Met  
100 105 110  
Ala Asn Leu Ala Leu Ala Asp Leu Leu Ser Val Ile Trp Phe Pro Leu  
115 120 125  
Lys Ile Ser Tyr His Leu His Gly Asn Asn Trp Val Tyr Gly Glu Ala  
130 135 140  
Leu Cys Lys Val Leu Ile Gly Phe Phe Tyr Gly Asn Met Tyr Cys Ser  
145 150 155 160  
Ile Leu Phe Met Thr Cys Leu Ser Val Gln Arg Tyr Trp Val Ile Val  
165 170 175  
Asn Pro Met Gly His Pro Arg Lys Lys Ala Asn Ile Ala Val Gly Val  
180 185 190  
Ser Leu Ala Ile Trp Leu Leu Ile Phe Leu Val Thr Ile Pro Leu Tyr  
195 200 205  
Val Met Lys Gln Thr Ile Tyr Ile Pro Ala Leu Asn Ile Thr Thr Cys  
210 215 220  
His Asp Val Leu Pro Glu Glu Val Leu Val Gly Asp Met Phe Asn Tyr  
225 230 235 240





Tyr Cys Ser Ile Leu Phe Met Thr Cys Leu Ser Val Gln Arg Tyr Trp  
 165 170 175  
 Val Ile Val Asn Pro Met Gly His Ser Arg Lys Lys Ala Asn Ile Ala  
 180 185 190  
 Ile Gly Ile Ser Leu Ala Ile Trp Leu Leu Ile Leu Leu Val Thr Ile  
 195 200 205  
 Pro Leu Tyr Val Val Lys Gln Thr Ile Phe Ile Pro Ala Leu Asn Ile  
 210 215 220  
 Thr Thr Cys His Asp Val Leu Pro Glu Gln Leu Leu Val Gly Asp Met  
 225 230 235 240  
 Phe Asn Tyr Phe Leu Ser Leu Ala Ile Gly Val Phe Leu Phe Pro Ala  
 245 250 255  
 Phe Leu Thr Ala Ser Ala Tyr Val Leu Met Ile Arg Met Leu Arg Ser  
 260 265 270  
 Ser Ala Met Asp Glu Asn Ser Glu Lys Lys Arg Lys Arg Ala Ile Lys  
 275 280 285  
 Leu Ile Val Thr Val Leu Ala Met Tyr Leu Ile Cys Phe Ile Pro Ser  
 290 295 300  
 Asn Leu Leu Leu Val Val His Tyr Phe Leu Ile Lys Ser Gln Gly Gln  
 305 310 315 320  
 Ser His Val Tyr Ala Leu Tyr Ile Val Ala Leu Cys Leu Ser Thr Leu  
 325 330 335  
 Asn Ser Cys Ile Asp Pro Phe Val Tyr Tyr Phe Val Ser His Asp Phe  
 340 345 350  
 Arg Asp His Ala Lys Asn Ala Leu Leu Cys Arg Ser Val Arg Thr Val  
 355 360 365  
 Lys Gln Met Gln Val Ser Leu Ile Ser Lys Lys His Ser Arg Lys Ser  
 370 375 380  
 Ser Ser Tyr Ser Ser Ser Ser Thr Thr Val Lys Thr Ser Tyr  
 385 390 395

<210> 7  
 <211> 425  
 <212> PRT  
 <213> Mus musculus

<220>  
 <223> Thrombin receptor

<400> 7  
 Met Gly Pro Arg Arg Leu Leu Leu Val Ala Ala Cys Phe Ser Leu Cys  
 1 5 10 15  
 Gly Phe Leu Leu Ser Ala Arg Thr Arg Ala Arg Arg Pro Glu Ser Lys  
 20 25 30  
 Ala Thr Asn Ala Thr Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro  
 35 40 45  
 Asn Asp Lys Tyr Glu Pro Phe Trp Glu Asp Glu Glu Lys Asn Glu Ser  
 50 55 60  
 Gly Leu Thr Glu Tyr Arg Leu Val Ser Ile Asn Lys Ser Ser Pro Leu  
 65 70 75 80

Gln	Lys	Gln	Leu	Pro	Ala	Phe	Ile	Ser	Glu	Asp	Ala	Ser	Gly	Tyr	Leu	
				85					90					95		
Thr	Ser	Ser	Trp	Leu	Thr	Leu	Phe	Val	Pro	Ser	Val	Tyr	Thr	Gly	Val	
			100					105					110			
Phe	Val	Val	Ser	Leu	Pro	Leu	Asn	Ile	Met	Ala	Ile	Val	Val	Phe	Ile	
		115					120					125				
Leu	Lys	Met	Lys	Val	Lys	Lys	Pro	Ala	Val	Val	Tyr	Met	Leu	His	Leu	
	130					135					140					
Ala	Thr	Ala	Asp	Val	Leu	Phe	Val	Ser	Val	Leu	Pro	Phe	Lys	Ile	Ser	
145					150					155					160	
Tyr	Tyr	Phe	Ser	Gly	Ser	Asp	Trp	Gln	Phe	Gly	Ser	Glu	Leu	Cys	Arg	
				165					170					175		
Phe	Val	Thr	Ala	Ala	Phe	Tyr	Cys	Asn	Met	Tyr	Ala	Ser	Ile	Leu	Leu	
			180					185					190			
Met	Thr	Val	Ile	Ser	Ile	Asp	Arg	Phe	Leu	Ala	Val	Val	Tyr	Pro	Met	
		195					200					205				
Gln	Ser	Leu	Ser	Trp	Arg	Thr	Leu	Gly	Arg	Ala	Ser	Phe	Thr	Cys	Leu	
	210					215					220					
Ala	Ile	Trp	Ala	Leu	Ala	Ile	Ala	Gly	Val	Val	Pro	Leu	Val	Leu	Lys	
225					230					235					240	
Glu	Gln	Thr	Ile	Gln	Val	Pro	Gly	Leu	Asn	Ile	Thr	Thr	Cys	His	Asp	
				245					250					255		
Val	Leu	Asn	Glu	Thr	Leu	Leu	Glu	Gly	Tyr	Tyr	Ala	Tyr	Tyr	Phe	Ser	
			260					265					270			
Ala	Phe	Ser	Ala	Val	Phe	Phe	Phe	Val	Pro	Leu	Ile	Ile	Ser	Thr	Val	
		275					280					285				
Cys	Tyr	Val	Ser	Ile	Ile	Arg	Cys	Leu	Ser	Ser	Ser	Ala	Val	Ala	Asn	
	290					295					300					
Arg	Ser	Lys	Lys	Ser	Arg	Ala	Leu	Phe	Leu	Ser	Ala	Ala	Val	Phe	Cys	
305					310					315					320	
Ile	Phe	Ile	Ile	Cys	Phe	Gly	Pro	Thr	Asn	Val	Leu	Leu	Ile	Ala	His	
				325					330					335		
Tyr	Ser	Phe	Leu	Ser	His	Thr	Ser	Thr	Thr	Glu	Ala	Ala	Tyr	Phe	Ala	
			340					345					350			
Tyr	Leu	Leu	Cys	Val	Cys	Val	Ser	Ser	Ile	Ser	Ser	Cys	Ile	Asp	Pro	
		355					360					365				
Leu	Ile	Tyr	Tyr	Tyr	Ala	Ser	Ser	Glu	Cys	Gln	Arg	Tyr	Val	Tyr	Ser	
	370					375					380					
Ile	Leu	Cys	Cys	Lys	Glu	Ser	Ser	Asp	Pro	Ser	Ser	Tyr	Asn	Ser	Ser	
385					390					395					400	
Gly	Gln	Leu	Met	Ala	Ser	Lys	Met	Asp	Thr	Cys	Ser	Ser	Asn	Leu	Asn	
				405					410					415		
Asn	Ser	Ile	Tyr	Lys	Lys	Leu	Leu	Thr								
			420					425								

<210> 8  
<211> 7

<212> PRT  
<213> Mus musculus

<220>  
<223> C140 receptor activation peptide

<400> 8  
Arg Asn Asn Ser Lys Gly Arg  
1 5

<210> 9  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<221> VARIANT  
<222> (1)  
<223> Xaa at position 1 = 3-mercaptopropionic acid

<220>  
<223> Description of Artificial Sequence: C140 receptor  
antagonist

<400> 9  
Xaa Leu Leu Gly Lys  
1 5

<210> 10  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140  
antagonist

<220>  
<221> VARIANT  
<222> (1)  
<223> Xaa at position 1 = 3-mercaptopropionic acid

<400> 10  
Xaa Leu Ile Gly Arg  
1 5

<210> 11  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor  
antagonist

<220>  
<221> VARIANT  
<222> (1)..(2)  
<223> Xaa at position 1 = 3-mercaptopropionic acid; Xaa  
at position 2 = cyclohexylalanine

<400> 11  
Xaa Xaa Leu Lys Gly  
1 5

<210> 12

<211> 5  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: C140 receptor antagonist  
  
 <220>  
 <221> VARIANT  
 <222> (1)..(2)  
 <223> Xaa at position 1 = 3-mercaptopropionic acid; Xaa at position 2 = cyclohexylalanine  
  
 <400> 12  
 Xaa Xaa Ile Gly Arg  
   1                  5  
  
 <210> 13  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: C140 receptor antagonist  
  
 <220>  
 <221> VARIANT  
 <222> (1)  
 <223> Xaa at position 1 = 3-mercaptopropionic acid  
  
 <400> 13  
 Xaa Leu Leu Gly Lys Lys  
   1                  5  
  
 <210> 14  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: C140 receptor antagonist  
  
 <220>  
 <221> VARIANT  
 <222> (1)  
 <223> Xaa at position 1 = 3-mercaptopropionic acid  
  
 <400> 14  
 Xaa Leu Ile Gly Arg Lys  
   1                  5  
  
 <210> 15  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: C140 receptor antagonist  
  
 <220>  
 <221> VARIANT  
 <222> (1)  
 <223> Xaa at position 1 = 3-mercaptopropionic acid

<400> 15  
 Xaa Leu Ile Gly Arg Lys Glu Thr Gln Pro  
       1                      5                      10

<210> 16  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: C140 receptor antagonist

<220>  
 <221> VARIANT  
 <222> (1)  
 <223> Xaa at position 1 = 3-mercaptopropionic acid

<400> 16  
 Xaa Leu Leu Gly Lys Lys Asp Gly Thr Ser  
       1                      5                      10

<210> 17  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: C140 receptor antagonist

<220>  
 <221> VARIANT  
 <222> (1)  
 <223> Xaa at position 1 = (n-pentyl) 2-N-Leu

<400> 17  
 Xaa Ile Gly Arg Lys  
       1                      5

<210> 18  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: C140 receptor antagonist

<220>  
 <221> VARIANT  
 <222> (1)  
 <223> Xaa at position 1 = Me-N-(n-pentyl)

<400> 18  
 Xaa Leu Ile Gly Arg Lys  
       1                      5

<210> 19  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: C140 receptor

agonist/immunogen

<400> 19

Ser Lys Gly Arg Ser Leu Ile Gly Arg Leu Glu Thr  
1 5 10

<210> 20

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: C140 receptor  
agonist/immunogen

<400> 20

Ile Ser Tyr His Leu His Gly Asn Asn Trp Val Tyr Gly Glu Ala Leu  
1 5 10 15

Cys

<210> 21

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: C140 receptor  
agonist/immunogen

<400> 21

Gln Thr Ile Tyr Ile Pro Ala Leu Asn Ile Thr Thr Cys His Asp Val  
1 5 10 15

Leu Pro Glu Glu Val Leu Val Gly Asp Met Phe Asn Tyr Phe Leu  
20 25 30

<210> 22

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: C140 receptor  
agonist/immunogen

<400> 22

His Tyr Phe Leu Ile Lys Thr Gln Arg Gln Ser His Val Tyr Ala  
1 5 10 15

<210> 23

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: C140 receptor  
agonist

<400> 23

Ser Leu Ile Gly Arg Leu  
1 5

<210> 24

<211> 6  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: C140 receptor agonist  
  
 <400> 24  
 Ser Leu Ile Gly Arg Ala  
   1                  5  
  
 <210> 25  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: C140 receptor agonist  
  
 <400> 25  
 Ser Leu Ile Gly Ala Leu  
   1                  5  
  
 <210> 26  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: C140 receptor agonist  
  
 <400> 26  
 Ser Leu Ile Ala Arg Leu  
   1                  5  
  
 <210> 27  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: C140 receptor agonist  
  
 <400> 27  
 Ser Leu Ala Gly Arg Leu  
   1                  5  
  
 <210> 28  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: C140 receptor agonist  
  
 <400> 28  
 Ser Ala Ile Gly Arg Leu  
   1                  5  
  
 <210> 29

<211> 6  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: C140 receptor agonist  
  
 <400> 29  
 Ala Leu Ile Gly Arg Leu  
   1                  5  
  
  
 <210> 30  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: C140 receptor agonist  
  
 <400> 30  
 Ser Phe Phe Leu Arg Trp  
   1                  5  
  
  
 <210> 31  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: C140 receptor agonist  
  
 <400> 31  
 Arg Asn Asn Ser Ser Lys Gly Arg  
   1                  5  
  
  
 <210> 32  
 <211> 13  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: C140 receptor agonist  
  
 <400> 32  
 Ser Leu Ile Gly Arg Leu Glu Thr Gln Pro Pro Ile Thr  
   1                  5                  10  
  
  
 <210> 33  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: C140 receptor agonist  
  
 <400> 33  
 Ser Leu Ile Gly Arg Leu Glu Thr Gln Pro Pro Ile  
   1                  5                  10  
  
  
 <210> 34



<211> 11  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: C140 receptor agonist  
  
 <400> 34  
 Ser Leu Ile Gly Arg Leu Glu Thr Gln Pro Pro  
   1                  5                  10  
  
 <210> 35  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: C140 receptor agonist  
  
 <400> 35  
 Ser Leu Ile Gly Arg Leu Glu Thr Gln Pro  
   1                  5                  10  
  
 <210> 36  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: C140 receptor agonist  
  
 <400> 36  
 Ser Leu Ile Gly Arg Leu Glu Thr Gln  
   1                  5  
  
 <210> 37  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: C140 agonist  
  
 <400> 37  
 Ser Leu Ile Gly Arg Leu Glu Thr  
   1                  5  
  
 <210> 38  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: C140 receptor agonist  
  
 <400> 38  
 Ser Leu Ile Gly Arg Leu Glu  
   1                  5  
  
 <210> 39  
 <211> 6

<212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: C140 receptor agonist  
  
 <400> 39  
 Ser Leu Ile Gly Arg Leu  
     1                    5  
  
 <210> 40  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: C140 receptor agonist  
  
 <400> 40  
 Ser Leu Ile Gly Arg  
     1                    5  
  
 <210> 41  
 <211> 13  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: C140 receptor agonist  
  
 <400> 41  
 Ser Leu Leu Gly Lys Val Asp Gly Thr Ser His Val Thr  
     1                    5                    10  
  
 <210> 42  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: C140 receptor agonist  
  
 <400> 42  
 Ser Leu Leu Gly Lys Val Asp Gly Thr Ser His Val  
     1                    5                    10  
  
 <210> 43  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: C140 receptor agonist  
  
 <400> 43  
 Ser Leu Leu Gly Lys Val Asp Gly Thr Ser His  
     1                    5                    10  
  
 <210> 44  
 <211> 10

<212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: C140 receptor agonist  
  
 <400> 44  
 Ser Leu Leu Gly Lys Val Asp Gly Thr Ser  
       1                              5                              10  
  
 <210> 45  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: C140 receptor agonist  
  
 <400> 45  
 Ser Leu Leu Gly Lys Val Asp Gly Thr  
       1                              5  
  
 <210> 46  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: C140 receptor agonist  
  
 <400> 46  
 Ser Leu Leu Gly Lys Val Asp Gly  
       1                              5  
  
 <210> 47  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: C140 receptor agonist  
  
 <400> 47  
 Ser Leu Leu Gly Lys Val Asp  
       1                              5  
  
 <210> 48  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: C140 receptor agonist  
  
 <400> 48  
 Ser Leu Leu Gly Lys Val  
       1                              5  
  
 <210> 49  
 <211> 5

<212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: C140 receptor agonist  
  
 <400> 49  
 Ser Leu Leu Gly Lys  
   1                  5  
  
 <210> 50  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: C140 receptor agonist  
  
 <220>  
 <221> VARIANT  
 <222> (2)  
 <223> Xaa at position 2 = cyclohexylalanine (Cha)  
  
 <400> 50  
 Ser Xaa Ile Gly Arg  
   1                  5  
  
 <210> 51  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: C140 receptor agonist  
  
 <220>  
 <221> VARIANT  
 <222> (2)  
 <223> Xaa at position 2 = cyclohexylalanine (Cha)  
  
 <400> 51  
 Ser Xaa Leu Gly Lys  
   1                  5  
  
 <210> 52  
 <211> 4  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: C140 receptor agonist  
  
 <220>  
 <221> VARIANT  
 <222> (1)  
 <223> Xaa at position 1 = 2,3-diamino propionic acid (2,3-diaP)  
  
 <400> 52  
 Xaa Ile Gly Arg  
   1

<210> 53  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: C140 receptor agonist  
  
 <220>  
 <221> VARIANT  
 <222> (1)  
 <223> Xaa at position 1 = 2,3-diamino propionic acid (2,3-diaP)  
  
 <400> 53  
 Xaa Leu Leu Gly Lys  
   1                  5  
  
 <210> 54  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: C140 receptor agonist  
  
 <400> 54  
 Ser Leu Leu Gly Lys Arg  
   1                  5  
  
 <210> 55  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: C140 receptor agonist  
  
 <400> 55  
 Ser Leu Ile Gly Arg Arg  
   1                  5  
  
 <210> 56  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: C140 receptor agonist  
  
 <220>  
 <221> VARIANT  
 <222> (2)  
 <223> Xaa at position 2= cyclohexylalanine (Cha)  
  
 <400> 56  
 Ser Xaa Leu Gly Lys Lys  
   1                  5  
  
 <210> 57  
 <211> 6  
 <212> PRT

```

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: C140 agonist
      receptor

<220>
<221> VARIANT
<222> (2)
<223> Xaa at position 2 = cyclohexylalanine (Cha)

<400> 57
Ser Xaa Ile Gly Arg Lys
  1                               5

<210> 58
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: C140 receptor
      agonist

<220>
<221> VARIANT
<222> (1)
<223> Xaa at position 1 = 2,3-diamino propionic acid
      (2,3-diaP)

<400> 58
Xaa Leu Ile Gly Arg Lys
  1                               5

<210> 59
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: C140 receptor
      agonist

<220>
<221> VARIANT
<222> (1)
<223> Xaa at position 1 = 2,3-diamino propionic acid
      (2,3-diaP)

<400> 59
Xaa Leu Leu Gly Lys Lys
  1                               5

<210> 60
<211> 2732
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (73)..(1269)
<223> C140 receptor, cDNA and deduced protein sequences

<400> 60
ccctgtgctc agagtagggc tccgagtttc gaaccactgg tggcggattg cccgcccgcc 60
ccacgtccgg gg atg cga agt ctc agc ctg gcg tgg ctg ctg gga ggt atc 111

```

	Met	Arg	Ser	Leu	Ser	Leu	Ala	Trp	Leu	Leu	Gly	Gly	Ile	
	1				5					10				
acc ctt ctg gcg gcc tcg gtc tcc tgc agc cgg acc gag aac ctt gca	159													
Thr Leu Leu Ala Ala Ser Val Ser Cys Ser Arg Thr Glu Asn Leu Ala														
15 20 25														
ccg gga cgc aac aac agt aaa gga aga agt ctt att ggc aga tta gaa	207													
Pro Gly Arg Asn Asn Ser Lys Gly Arg Ser Leu Ile Gly Arg Leu Glu														
30 35 40 45														
acc cag cct cca atc act ggg aaa ggg gtt ccg gta gaa cca ggc ttt	255													
Thr Gln Pro Pro Ile Thr Gly Lys Gly Val Pro Val Glu Pro Gly Phe														
50 55 60														
tcc atc gat gag ttc tct gcg tcc atc ctc acc ggg aag ctg acc acg	303													
Ser Ile Asp Glu Phe Ser Ala Ser Ile Leu Thr Gly Lys Leu Thr Thr														
65 70 75														
gtc ttt ctt ccg gtc gtc tac att att gtg ttt gtg att ggt ttg ccc	351													
Val Phe Leu Pro Val Val Tyr Ile Ile Val Phe Val Ile Gly Leu Pro														
80 85 90														
agt aat ggc atg gcc ctc tgg atc ttc ctt ttc cga acg aag aag aaa	399													
Ser Asn Gly Met Ala Leu Trp Ile Phe Leu Phe Arg Thr Lys Lys Lys														
95 100 105														
cac ccc gcc gtg att tac atg gcc aac ctg gcc ttg gcc gac ctc ctc	447													
His Pro Ala Val Ile Tyr Met Ala Asn Leu Ala Leu Ala Asp Leu Leu														
110 115 120 125														
tct gtc atc tgg ttc ccc ctg aag atc tcc tac cac cta cat ggc aac	495													
Ser Val Ile Trp Phe Pro Leu Lys Ile Ser Tyr His Leu His Gly Asn														
130 135 140														
aac tgg gtc tac ggg gag gcc ctg tgc aag gtg ctc att ggc ttt ttc	543													
Asn Trp Val Tyr Gly Glu Ala Leu Cys Lys Val Leu Ile Gly Phe Phe														
145 150 155														
tat ggt aac atg tat tgc tcc atc ctc ttc atg acc tgc ctc agc gtg	591													
Tyr Gly Asn Met Tyr Cys Ser Ile Leu Phe Met Thr Cys Leu Ser Val														
160 165 170														
cag agg tac tgg gtg atc gtg aac ccc atg gga cac ccc agg aag aag	639													
Gln Arg Tyr Trp Val Ile Val Asn Pro Met Gly His Pro Arg Lys Lys														
175 180 185														
gca aac atc gcc gtt ggc gtc tcc ttg gca atc tgg ctc ctg att ttt	687													
Ala Asn Ile Ala Val Gly Val Ser Leu Ala Ile Trp Leu Leu Ile Phe														
190 195 200 205														
ctg gtc acc atc cct ttg tat gtc atg aag cag acc atc tac att cca	735													
Leu Val Thr Ile Pro Leu Tyr Val Met Lys Gln Thr Ile Tyr Ile Pro														
210 215 220														
gca ttg aac atc acc acc tgt cac gat gtg ctg cct gag gag gta ttg	783													
Ala Leu Asn Ile Thr Thr Cys His Asp Val Leu Pro Glu Glu Val Leu														
225 230 235														
gtg ggg gac atg ttc aat tac ttc ctc tca ctg gcc att gga gtc ttc	831													
Val Gly Asp Met Phe Asn Tyr Phe Leu Ser Leu Ala Ile Gly Val Phe														
240 245 250														
ctg ttc ccg gcc ctc ctt act gca tct gcc tac gtg ctc atg atc aag	879													
Leu Phe Pro Ala Leu Leu Thr Ala Ser Ala Tyr Val Leu Met Ile Lys														
255 260 265														
acg ctc cgc tct tct gct atg gat gaa cac tca gag aag aaa agg cag	927													
Thr Leu Arg Ser Ser Ala Met Asp Glu His Ser Glu Lys Lys Arg Gln														
270 275 280 285														

agg gct atc cga ctc atc atc acc gtg ctg gcc atg tac ttc atc tgc 975  
 Arg Ala Ile Arg Leu Ile Ile Thr Val Leu Ala Met Tyr Phe Ile Cys  
 290 295 300

ttt gct cct agc aac ctt ctg ctc gta gtg cat tat ttc cta atc aaa 1023  
 Phe Ala Pro Ser Asn Leu Leu Leu Val Val His Tyr Phe Leu Ile Lys  
 305 310 315

acc cag agg cag agc cac gtc tac gcc ctc tac ctt gtc gcc ctc tgc 1071  
 Thr Gln Arg Gln Ser His Val Tyr Ala Leu Tyr Leu Val Ala Leu Cys  
 320 325 330

ctg tcg acc ctc aac agc tgc ata gac ccc ttt gtc tat tac ttt gtc 1119  
 Leu Ser Thr Leu Asn Ser Cys Ile Asp Pro Phe Val Tyr Tyr Phe Val  
 335 340 345

tca aaa gat ttc agg gat cac gcc aga aac gcg ctc ctc tgc cga agt 1167  
 Ser Lys Asp Phe Arg Asp His Ala Arg Asn Ala Leu Leu Cys Arg Ser  
 350 355 360 365

gtc cgc act gtg aat cgc atg caa atc tcg ctc agc tcc aac aag ttc 1215  
 Val Arg Thr Val Asn Arg Met Gln Ile Ser Leu Ser Ser Asn Lys Phe  
 370 375 380

tcc agg aag tcc ggc tcc tac tct tca agc tca acc agt gtt aaa acc 1263  
 Ser Arg Lys Ser Gly Ser Tyr Ser Ser Ser Thr Ser Val Lys Thr  
 385 390 395

tcc tac tgagctgtac ctgaggatgt caagcctgct tgatgatgat gatgatgatg 1319  
 Ser Tyr

gtgtgtgtgt gtgtgtgtgt gtgtgtgtgt gtgtgtgtgt gcacccgtgt gtgagtgcgt 1379

ggtagggata caccaacatg gatggggctg tcatttccta tccaagctgt ctgtctctgc 1439

accaatcaca agcatgcagc tctccccagg attgacagaa gcctcctcct ttgcatgaga 1499

acagtcttcc actctgatga aaagcatcag tatcagaaac tgaaacgaac tgagaggagc 1559

ttgttttgtg aaagtgaaga gaagatggag ggtcagtgac ttgcaaaaaa aaccaaccaa 1619

acaaaaaacta cacctggcaa gaaggctaag actctctgaa atgcttccct tttccatctg 1679

gagttcgtct cggccttggt caggacctga ggccctggta gagcttcagt ccagttgatt 1739

gactttacag acttgagaga ggagtgaatg aggagtgaat gaggctcctg gcggcatcct 1799

aaccggctaa cagtggcctt gctggacaat aggattcaga tggctggagt tacattctca 1859

caccatttca tcagaactat tggggatcct gatcaatgtg cagggtccctt agcgtcagta 1919

accctgggag ctcagacacg atgggggtga ggggtgggggt gggggtgggg gtgaggctct 1979

acaaacccta gtgatgactg cagacacaga accatggagc tgagcctgct tctgcttgcc 2039

agggcaccac tgtaatgttg gcaaagaaaa accaacagca gtgttttgag cctctttttt 2099

tggtcagttt atgatgaatt tgcctattgg tttattggga ttttcagttc ctttattact 2159

ttgttgtaat tttgtgtgtt tattagtcaa gaaaaagaag atgaggctct taaaaatgta 2219

aataaaattt ttggtttttt ggttttttaa cttgggccaa ctacaaatac tgcttaggtt 2279

tttttctaac ttaattgtta actacatcat gtgaacttaa gacattttca tgataaagca 2339

ttactgtagt gtcagttttc cctcatcctc gatcatagtc cttcccgtag agcagggccc 2399

ttccctccc ccccttttgc cgtttccctc cccaccagat agtccccctg tctgctttaa 2459



cctaccagtt agtattttat aaaaacagat cattggaata tttattatca gttttgttca 2519  
 cttgttatca gttttgttca ctaatttgtc caataatgga attaacgtct tctcatctgt 2579  
 ttgaggaaga tctgaaacaa ggggccattg caggagtaca tggctccagg cttactttat 2639  
 atactgcctg tatttgtggc tttaaaaaaa tgaccttgtt atatgaatgc tttataaata 2699  
 aataatgcat gaacttttaa aaaaaaaaaa aaa 2732

<210> 61  
 <211> 399  
 <212> PRT  
 <213> Mus musculus

<400> 61  
 Met Arg Ser Leu Ser Leu Ala Trp Leu Leu Gly Gly Ile Thr Leu Leu  
 1 5 10 15  
 Ala Ala Ser Val Ser Cys Ser Arg Thr Glu Asn Leu Ala Pro Gly Arg  
 20 25 30  
 Asn Asn Ser Lys Gly Arg Ser Leu Ile Gly Arg Leu Glu Thr Gln Pro  
 35 40 45  
 Pro Ile Thr Gly Lys Gly Val Pro Val Glu Pro Gly Phe Ser Ile Asp  
 50 55 60  
 Glu Phe Ser Ala Ser Ile Leu Thr Gly Lys Leu Thr Thr Val Phe Leu  
 65 70 75 80  
 Pro Val Val Tyr Ile Ile Val Phe Val Ile Gly Leu Pro Ser Asn Gly  
 85 90 95  
 Met Ala Leu Trp Ile Phe Leu Phe Arg Thr Lys Lys Lys His Pro Ala  
 100 105 110  
 Val Ile Tyr Met Ala Asn Leu Ala Leu Ala Asp Leu Leu Ser Val Ile  
 115 120 125  
 Trp Phe Pro Leu Lys Ile Ser Tyr His Leu His Gly Asn Asn Trp Val  
 130 135 140  
 Tyr Gly Glu Ala Leu Cys Lys Val Leu Ile Gly Phe Phe Tyr Gly Asn  
 145 150 155 160  
 Met Tyr Cys Ser Ile Leu Phe Met Thr Cys Leu Ser Val Gln Arg Tyr  
 165 170 175  
 Trp Val Ile Val Asn Pro Met Gly His Pro Arg Lys Lys Ala Asn Ile  
 180 185 190  
 Ala Val Gly Val Ser Leu Ala Ile Trp Leu Leu Ile Phe Leu Val Thr  
 195 200 205  
 Ile Pro Leu Tyr Val Met Lys Gln Thr Ile Tyr Ile Pro Ala Leu Asn  
 210 215 220  
 Ile Thr Thr Cys His Asp Val Leu Pro Glu Glu Val Leu Val Gly Asp  
 225 230 235 240  
 Met Phe Asn Tyr Phe Leu Ser Leu Ala Ile Gly Val Phe Leu Phe Pro  
 245 250 255  
 Ala Leu Leu Thr Ala Ser Ala Tyr Val Leu Met Ile Lys Thr Leu Arg  
 260 265 270  
 Ser Ser Ala Met Asp Glu His Ser Glu Lys Lys Arg Gln Arg Ala Ile  
 275 280 285

Arg Leu Ile Ile Thr Val Leu Ala Met Tyr Phe Ile Cys Phe Ala Pro  
 290 295 300  
 Ser Asn Leu Leu Leu Val Val His Tyr Phe Leu Ile Lys Thr Gln Arg  
 305 310 315 320  
 Gln Ser His Val Tyr Ala Leu Tyr Leu Val Ala Leu Cys Leu Ser Thr  
 325 330 335  
 Leu Asn Ser Cys Ile Asp Pro Phe Val Tyr Tyr Phe Val Ser Lys Asp  
 340 345 350  
 Phe Arg Asp His Ala Arg Asn Ala Leu Leu Cys Arg Ser Val Arg Thr  
 355 360 365  
 Val Asn Arg Met Gln Ile Ser Leu Ser Ser Asn Lys Phe Ser Arg Lys  
 370 375 380  
 Ser Gly Ser Tyr Ser Ser Ser Ser Thr Ser Val Lys Thr Ser Tyr  
 385 390 395

<210> 62  
 <211> 1414  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (50)..(1240)  
 <223> C140 receptor, cDNA and deduced protein sequences

<400> 62  
 caaagaattg taatagcact cactataggg cgaattcgga tccaggagg atg cgg agc 58  
 Met Arg Ser  
 1  
  
 ccc agc gcg gcg tgg ctg ctg ggg gcc gcc atc ctg cta gca gcc tct 106  
 Pro Ser Ala Ala Trp Leu Leu Gly Ala Ala Ile Leu Leu Ala Ala Ser  
 5 10 15  
  
 ctc tcc tgc agt ggc acc atc caa gga acc aat aga tcc tct aaa gga 154  
 Leu Ser Cys Ser Gly Thr Ile Gln Gly Thr Asn Arg Ser Ser Lys Gly  
 20 25 30 35  
  
 aga agc ctt att ggt aag gtt gat ggc aca tcc cac gtc act gga aaa 202  
 Arg Ser Leu Ile Gly Lys Val Asp Gly Thr Ser His Val Thr Gly Lys  
 40 45 50  
  
 gga gtt aca gtt gaa aca gtc ttt tct gtg gat gag ttt tct gca tct 250  
 Gly Val Thr Val Glu Thr Val Phe Ser Val Asp Glu Phe Ser Ala Ser  
 55 60 65  
  
 gtc ctc gct gga aaa ctg acc act gtc ttc ctt cca att gtc tac aca 298  
 Val Leu Ala Gly Lys Leu Thr Thr Val Phe Leu Pro Ile Val Tyr Thr  
 70 75 80  
  
 att gtg ttt gcg gtg ggt ttg cca agt aac ggc atg gcc cta tgg gtc 346  
 Ile Val Phe Ala Val Gly Leu Pro Ser Asn Gly Met Ala Leu Trp Val  
 85 90 95  
  
 ttt ctt ttc cga act aag aag aag cac cct gct gtg att tac atg gcc 394  
 Phe Leu Phe Arg Thr Lys Lys Lys His Pro Ala Val Ile Tyr Met Ala  
 100 105 110 115  
  
 aat ctg gcc ttg gct gac ctc ctc tct gtc atc tgg ttc ccc ttg aag 442  
 Asn Leu Ala Leu Ala Asp Leu Leu Ser Val Ile Trp Phe Pro Leu Lys  
 120 125 130

att gcc tat cac ata cat ggc aac aac tgg att tat ggg gaa gct ctt Ile Ala Tyr His Ile His Gly Asn Asn Trp Ile Tyr Gly Glu Ala Leu 135 140 145	490
tgt aat gtg ctt att ggc ttt ttc tat cgc aac atg tac tgt tcc att Cys Asn Val Leu Ile Gly Phe Phe Tyr Gly Asn Met Tyr Cys Ser Ile 150 155 160	538
ctc ttc atg acc tgc ctc agt gtg cag agg tat tgg gtc atc gtg aac Leu Phe Met Thr Cys Leu Ser Val Gln Arg Tyr Trp Val Ile Val Asn 165 170 175	586
ccc atg ggg cac tcc agg aag aag gca aac att gcc att ggc atc tcc Pro Met Gly His Ser Arg Lys Lys Ala Asn Ile Ala Ile Gly Ile Ser 180 185 190 195	634
ctg gca ata tgg ctg ctg act ctg ctg gtc acc atc cct ttg tat gtc Leu Ala Ile Trp Leu Leu Thr Leu Leu Val Thr Ile Pro Leu Tyr Val 200 205 210	682
gtg aag cag acc atc ttc att cct gcc ctg aac atc acg acc tgt cat Val Lys Gln Thr Ile Phe Ile Pro Ala Leu Asn Ile Thr Thr Cys His 215 220 225	730
gat gtt ttg cct gag cag ctc ttg gtg gga gac atg ttc aat tac ttc Asp Val Leu Pro Glu Gln Leu Leu Val Gly Asp Met Phe Asn Tyr Phe 230 235 240	778
ctc tct ctg gcc att ggg gtc ttt ctg ttc cca gcc ttc ctc aca gcc Leu Ser Leu Ala Ile Gly Val Phe Leu Phe Pro Ala Phe Leu Thr Ala 245 250 255	826
tct gcc tat gtg ctg atg atc aga atg ctg cga tct tct gcc atg gat Ser Ala Tyr Val Leu Met Ile Arg Met Leu Arg Ser Ser Ala Met Asp 260 265 270 275	874
gaa aac tca gag aag aaa agg aag agg gcc atc aaa ctc att gtc act Glu Asn Ser Glu Lys Lys Arg Lys Arg Ala Ile Lys Leu Ile Val Thr 280 285 290	922
gtc ctg ggc atg tac ctg atc tgc ttc act cct agt aac ctt ctg ctt Val Leu Gly Met Tyr Leu Ile Cys Phe Thr Pro Ser Asn Leu Leu 295 300 305	970
gtg gtg cat tat ttt ctg att aag agc cag ggc cag agc cat gtc tat Val Val His Tyr Phe Leu Ile Lys Ser Gln Gly Gln Ser His Val Tyr 310 315 320	1018
gcc ctg tac att gta gcc ctc tgc ctc tct acc ctt aac agc tgc atc Ala Leu Tyr Ile Val Ala Leu Cys Leu Ser Thr Leu Asn Ser Cys Ile 325 330 335	1066
gac ccc ttt gtc tat tac ttt gtt tca cat gat ttc agg gat cat gca Asp Pro Phe Val Tyr Tyr Phe Val Ser His Asp Phe Arg Asp His Ala 340 345 350 355	1114
aag aac gct ctc ctt tgc cga agt gtc cgc act gta aag cag atg caa Lys Asn Ala Leu Leu Cys Arg Ser Val Arg Thr Val Lys Gln Met Gln 360 365 370	1162
gta ccc ctc acc tca aag aaa cac tcc agg aaa tcc agc tct tac tct Val Pro Leu Thr Ser Lys Lys His Ser Arg Lys Ser Ser Ser Tyr Ser 375 380 385	1210
tca agt tca acc act gtt aag acc tcc tat tgagttttcc aggtcctcag Ser Ser Ser Thr Thr Val Lys Thr Ser Tyr 390 395	1260
atgggaattg cacagtagga tgtggaacct gtttaatggt atgaggacgt gtctgttatt	1320

tccggatcca gatcttatta aagcagaact tgtttattgc agcttataat ggttacaaat 1380  
 aaagcaatag catcacaaat ttcacaaata aagc 1414

<210> 63  
 <211> 397  
 <212> PRT  
 <213> Homo sapiens

<400> 63  
 Met Arg Ser Pro Ser Ala Ala Trp Leu Leu Gly Ala Ala Ile Leu Leu  
 1 5 10 15  
 Ala Ala Ser Leu Ser Cys Ser Gly Thr Ile Gln Gly Thr Asn Arg Ser  
 20 25 30  
 Ser Lys Gly Arg Ser Leu Ile Gly Lys Val Asp Gly Thr Ser His Val  
 35 40 45  
 Thr Gly Lys Gly Val Thr Val Glu Thr Val Phe Ser Val Asp Glu Phe  
 50 55 60  
 Ser Ala Ser Val Leu Ala Gly Lys Leu Thr Thr Val Phe Leu Pro Ile  
 65 70 75 80  
 Val Tyr Thr Ile Val Phe Ala Val Gly Leu Pro Ser Asn Gly Met Ala  
 85 90 95  
 Leu Trp Val Phe Leu Phe Arg Thr Lys Lys Lys His Pro Ala Val Ile  
 100 105 110  
 Tyr Met Ala Asn Leu Ala Leu Ala Asp Leu Leu Ser Val Ile Trp Phe  
 115 120 125  
 Pro Leu Lys Ile Ala Tyr His Ile His Gly Asn Asn Trp Ile Tyr Gly  
 130 135 140  
 Glu Ala Leu Cys Asn Val Leu Ile Gly Phe Phe Tyr Gly Asn Met Tyr  
 145 150 155 160  
 Cys Ser Ile Leu Phe Met Thr Cys Leu Ser Val Gln Arg Tyr Trp Val  
 165 170 175  
 Ile Val Asn Pro Met Gly His Ser Arg Lys Lys Ala Asn Ile Ala Ile  
 180 185 190  
 Gly Ile Ser Leu Ala Ile Trp Leu Leu Thr Leu Leu Val Thr Ile Pro  
 195 200 205  
 Leu Tyr Val Val Lys Gln Thr Ile Phe Ile Pro Ala Leu Asn Ile Thr  
 210 215 220  
 Thr Cys His Asp Val Leu Pro Glu Gln Leu Leu Val Gly Asp Met Phe  
 225 230 235 240  
 Asn Tyr Phe Leu Ser Leu Ala Ile Gly Val Phe Leu Phe Pro Ala Phe  
 245 250 255  
 Leu Thr Ala Ser Ala Tyr Val Leu Met Ile Arg Met Leu Arg Ser Ser  
 260 265 270  
 Ala Met Asp Glu Asn Ser Glu Lys Lys Arg Lys Arg Ala Ile Lys Leu  
 275 280 285  
 Ile Val Thr Val Leu Gly Met Tyr Leu Ile Cys Phe Thr Pro Ser Asn  
 290 295 300  
 Leu Leu Leu Val Val His Tyr Phe Leu Ile Lys Ser Gln Gly Gln Ser

305                      310                      315                      320  
 His Val Tyr Ala Leu Tyr Ile Val Ala Leu Cys Leu Ser Thr Leu Asn  
                                  325                                   330                                   335  
 Ser Cys Ile Asp Pro Phe Val Tyr Tyr Phe Val Ser His Asp Phe Arg  
                                  340                                   345                                   350  
 Asp His Ala Lys Asn Ala Leu Leu Cys Arg Ser Val Arg Thr Val Lys  
                                  355                                   360                                   365  
 Gln Met Gln Val Pro Leu Thr Ser Lys Lys His Ser Arg Lys Ser Ser  
                                  370                                   375                                   380  
 Ser Tyr Ser Ser Ser Ser Thr Thr Val Lys Thr Ser Tyr  
                                  385                                   390                                   395

<210> 64  
 <211> 424  
 <212> PRT  
 <213> Homo sapiens

<400> 64  
 Met Gly Pro Arg Arg Leu Leu Leu Val Ala Ala Cys Phe Ser Leu Cys  
                                  1                                   5                                   10                                   15  
 Gly Pro Leu Leu Ser Ala Arg Thr Arg Ala Arg Arg Pro Glu Ser Lys  
                                  20                                   25                                   30  
 Ala Thr Asn Ala Thr Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro  
                                  35                                   40                                   45  
 Asn Asp Lys Tyr Glu Pro Glu Trp Glu Asp Glu Glu Lys Asn Glu Ser  
                                  50                                   55                                   60  
 Gly Leu Thr Glu Tyr Arg Leu Val Ser Ile Asn Lys Ser Ser Pro Leu  
                                  65                                   70                                   75                                   80  
 Gln Lys Gln Leu Pro Ala Phe Ile Ser Glu Asp Ala Ser Gly Tyr Leu  
                                  85                                   90                                   95  
 Thr Ser Ser Trp Leu Thr Leu Phe Val Pro Ser Val Tyr Thr Gly Val  
                                  100                                   105                                   110  
 Phe Val Val Ser Leu Pro Leu Asn Ile Met Ala Ile Val Val Phe Ile  
                                  115                                   120                                   125  
 Leu Lys Met Lys Val Lys Lys Pro Ala Val Val Tyr Met Leu His Leu  
                                  130                                   135                                   140  
 Ala Thr Ala Asp Val Leu Phe Val Ser Val Leu Pro Phe Lys Ile Ser  
                                  145                                   150                                   155                                   160  
 Tyr Tyr Phe Ser Gly Ser Asp Trp Gln Phe Gly Ser Glu Leu Cys Arg  
                                  165                                   170                                   175  
 Phe Val Thr Ala Ala Phe Tyr Cys Asn Met Tyr Ala Ser Ile Leu Leu  
                                  180                                   185                                   190  
 Met Thr Val Ile Ser Ile Asp Arg Phe Leu Ala Val Val Tyr Pro Met  
                                  195                                   200                                   205  
 Gln Ser Leu Ser Trp Arg Thr Leu Gly Arg Ala Ser Phe Thr Cys Leu  
                                  210                                   215                                   220  
 Ala Ile Trp Ala Leu Ala Ile Ala Gly Val Val Pro Leu Val Leu Lys  
                                  225                                   230                                   235                                   240  
 Glu Gln Thr Ile Gln Val Pro Gly Leu Asn Ile Thr Thr Cys His Asp

245										250					255				
Val	Leu	Asn	Glu	Thr	Leu	Leu	Glu	Gly	Tyr	Tyr	Ala	Tyr	Tyr	Phe	Ser				
			260					265					270						
Ala	Phe	Ser	Ala	Val	Phe	Phe	Phe	Val	Pro	Leu	Ile	Ile	Ser	Thr	Val				
		275					280					285							
Cys	Tyr	Val	Ser	Ile	Ile	Arg	Cys	Leu	Ser	Ser	Ser	Ala	Val	Ala	Asn				
	290					295						300							
Arg	Ser	Lys	Lys	Ser	Arg	Ala	Leu	Phe	Leu	Ser	Ala	Ala	Val	Phe	Cys				
305					310					315					320				
Ile	Phe	Ile	Ile	Cys	Phe	Gly	Pro	Thr	Asn	Val	Leu	Leu	Ile	Ala	His				
				325					330					335					
Tyr	Ser	Phe	Leu	Ser	His	Thr	Ser	Thr	Thr	Glu	Ala	Ala	Tyr	Phe	Ala				
			340					345					350						
Tyr	Leu	Leu	Cys	Val	Cys	Val	Ser	Ser	Ile	Ser	Ser	Cys	Ile	Asp	Pro				
		355					360					365							
Leu	Ile	Tyr	Tyr	Tyr	Ala	Ser	Ser	Glu	Cys	Gln	Arg	Tyr	Val	Tyr	Ser				
	370					375					380								
Ile	Leu	Cys	Cys	Lys	Glu	Ser	Ser	Asp	Pro	Ser	Ser	Tyr	Asn	Ser	Ser				
385					390					395					400				
Gly	Gln	Leu	Met	Ala	Ser	Lys	Met	Asp	Thr	Cys	Ser	Ser	Asn	Leu	Asn				
				405					410					415					
Asn	Ser	Ile	Tyr	Lys	Lys	Leu	Leu	Thr											
				420															